```
357    Thr His Pro Gln Phe Arg Ser Ile Val Ser Ala Leu Lys Arg
358            1185            1190            1195
359
360    Glu Ala Leu Val Lys Gly Asn Pro Pro Ile Tyr Arg Phe Trp
361            1200            1205            1210
362
363    Lys Asp Asn Leu Gln His Lys Asp Ser Ser Val Pro Asn Thr
364            1215            1220
365
366    Gly Thr Ala Arg Met Val Glu Thr Thr Ala Tyr Ala Leu Leu
367    1225            1230            1235
368
369    Thr Ser Leu Asn Leu Lys Asp Ile Asn Tyr Val Asn Pro Val
370        1240            1245            1250
371
372    Ile Lys Trp Leu Ser Glu Glu Gln Arg Tyr Gly Gly Gly Phe
373            1255            1260            1265
374
375    Tyr Ser Thr Gln Asp Thr Ile Asn Ala Ile Glu Gly Leu Thr
376            1270            1275            1280
377
378    Glu Tyr Ser Leu Leu Val Lys Gln Leu Arg Leu Ser Met Asp
379            1285            1290
380
381    Ile Asp Val Ser Tyr Lys His Lys Gly Ala Leu His Asn Tyr
382    1295            1300            1305
383
384    Lys Met Thr Asp Lys Asn Phe Leu Gly Arg Pro Val Glu Val
385        1310            1315            1320
386
387    Leu Leu Asn Asp Asp Leu Ile Val Ser Thr Gly Phe Gly Ser
388            1325            1330            1335
389
390    Gly Leu Ala Thr Val His Val Thr Thr Val Val His Lys Thr
391            1340            1345            1350
392
393    Ser Thr Ser Glu Glu Val Cys Ser Phe Tyr Leu Lys Ile Asp
394            1355            1360
395
396    Thr Gln Asp Ile Glu Ala Ser His Tyr Arg Gly Tyr Gly Asn
397    1365            1370            1375
398
399    Ser Asp Tyr Lys Arg Ile Val Ala Cys Ala Ser Tyr Lys Pro
400        1380            1385            1390
401
402    Ser Arg Glu Glu Ser Ser Ser Gly Ser Ser His Ala Val Met
403            1395            1400            1405
404
405    Asp Ile Ser Leu Pro Thr Gly Ile Ser Ala Asn Glu Glu Asp
406            1410            1415            1420
407
408    Leu Lys Ala Leu Val Glu Gly Val Asp Gln Leu Phe Thr Asp
409            1425            1430
```

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410
411    Tyr Gln Ile Lys Asp Gly His Val Ile Leu Gln Leu Asn Ser
412    1435                1440                1445
413
414    Ile Pro Ser Ser Asp Phe Leu Cys Val Arg Phe Arg Ile Phe
415        1450                1455                1460
416
417    Glu Leu Phe Glu Val Gly Phe Leu Ser Pro Ala Thr Phe Thr
418            1465                1470                1475
419
420    Val Tyr Glu Tyr His Arg Pro Asp Lys Gln Cys Thr Met Phe
421            1480                1485                1490
422
423    Tyr Ser Thr Ser Asn Ile Lys Ile Gln Lys Val Cys Glu Gly
424                1495                1500
425
426    Ala Ala Cys Lys Cys Val Glu Ala Asp Cys Gly Gln Met Gln
427    1505                1510                1515
428
429    Glu Glu Leu Asp Leu Thr Ile Ser Ala Glu Thr Arg Lys Gln
430        1520                1525                1530
431
432    Thr Ala Cys Lys Pro Glu Ile Ala Tyr Ala Tyr Lys Val Ser
433            1535                1540                1545
434
435    Ile Thr Ser Ile Thr Val Glu Asn Val Phe Val Lys Tyr Lys
436                1550                1555                1560
437
438    Ala Thr Leu Leu Asp Ile Tyr Lys Thr Gly Glu Ala Val Ala
439                1565                1570
440
441    Glu Lys Asp Ser Glu Ile Thr Phe Ile Lys Lys Val Thr Cys
442    1575                1580                1585
443
444    Thr Asn Ala Glu Leu Val Lys Gly Arg Gln Tyr Leu Ile Met
445        1590                1595                1600
446
447    Gly Lys Glu Ala Leu Gln Ile Lys Tyr Asn Phe Ser Phe Arg
448            1605                1610                1615
449
450    Tyr Ile Tyr Pro Leu Asp Ser Leu Thr Trp Ile Glu Tyr Trp
451                1620                1625                1630
452
453    Pro Arg Asp Thr Thr Cys Ser Ser Cys Gln Ala Phe Leu Ala
454                1635                1640
455
456    Asn Leu Asp Glu Phe Ala Glu Asp Ile Phe Leu Asn Gly Cys
457    1645                1650                1655
458
459
460
```

```
2493    (2) INFORMATION FOR SEQ ID NO:19:
```

INPUT SET: S8120.raw

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        2494          (i) SEQUENCE CHARACTERISTICS:
-->     2495              (A) LENGTH:  813 base pairs      only 783 are
        2496              (B) TYPE:  Nucleic Acid                shown.
        2497              (C) STRANDEDNESS:  Double
        2498              (D) TOPOLOGY:  linear
        2499          (ii) MOLECULE TYPE:  Other nucleic acid
        2500              (A) DESCRIPTION: N19/8 scFv (His Tagged)
        2501
        2502
        2503     (xi) SEQUENCE DESCRIPTION:  SEQ ID NO:19:
        2504
        2505     ATG GCC AAT ATT GTG CTG ACC CAA TCT CCA 30
        2506     Met Ala Asn Ile Val Leu Thr Gln Ser Pro
        2507      1           5                   10
        2508
        2509     GCT TCT TTG GCT GTG TCT CTA GGG CAG AGG 60
        2510     Ala Ser Leu Ala Val Ser Leu Gly Gln Arg
        2511                 15                  20
        2512
-->     2513     GCC ACC ATA TCC TGC AGA GCC AGT GAA AGT 120   90?,
        2514     Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser
        2515                 25                  30
        2516
        2517     GTT GAT AGT TAT GAC AAT AGT TTT ATG CAC 150  ?
        2518     Val Asp Ser Tyr Asp Asn Ser Phe Met His
        2519                 35                  40
        2520
        2521     TGG TAC CAG CAG AAA CCA GGA CAG CCA CCC 180  ?
        2522     Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        2523                 45                  50
        2524
        2525     AAA CTC CTC ATC TTT CTT GCA TCC AAC CTA 210
        2526     Lys Leu Leu Ile Phe Leu Ala Ser Asn Leu
        2527                 55                  60
        2528
        2529     GAA TCT GGG GTC CCT GCC AGG TTC AGT GGC 240
        2530     Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
        2531                 65                  70
        2532
        2533     AGT GGG TCT AGG ACA GAC TTC ACC CTC ACC 270
        2534     Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr
        2535                 75                  80
        2536
        2537     ATT GAT CCT GTG GAG GCT GAT GAT GCT GCA 300
        2538     Ile Asp Pro Val Glu Ala Asp Asp Ala Ala
        2539                 85                  90
        2540
        2541     ACC TAT TAC TGT CAG CAA AAT AAT GAG GTT 330
        2542     Thr Tyr Tyr Cys Gln Gln Asn Asn Glu Val
        2543                 95                  100
        2544
        2545     CCG AAC ACG TTC GGA GGG GGG ACC AAG CTG 360
        2546     Pro Asn Thr Phe Gly Gly Gly Thr Lys Leu
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/236,208*

DATE: 01/05/96
TIME: 15:17:03

INPUT SET: S8120.raw

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2547                      105                 110
2548
2549  GAA ATA AAA CGG ACC GGA GGT GGC GGG TCG 390
2550  Glu Ile Lys Arg Thr Gly Gly Gly Gly Ser
2551                      115                 120
2552
2553  GGT GGC GGG GGA TCG GGT GGC GGA GGG TCG 420
2554  Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
2555                      125                 130
2556
2557  GAC GTC AAG CTC GTG GAG TCT GGG GGA GAC 450
2558  Asp Val Lys Leu Val Glu Ser Gly Gly Asp
2559                      135                 140
2560
2561  TTA GTG AAG CTT GGA GGG TCC CTG AAA CTC 480
2562  Leu Val Lys Leu Gly Gly Ser Leu Lys Leu
2563                      145                 150
2564
2565  TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT 510
2566  Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
2567                      155                 160
2568
2569  AGC TAT TAT ATG TCT TGG GTT CGC CAG ATT 540
2570  Ser Tyr Tyr Met Ser Trp Val Arg Gln Ile
2571                      165                 170
2572
2573  TCA GAG AAG AGG CTG GAG TTG GTC GCA GCC 570
2574  Ser Glu Lys Arg Leu Glu Leu Val Ala Ala
2575                      175                 180
2576
2577  ATT AAT AGT AAT GGT GAT AGC ACC TAC TAT 600
2578  Ile Asn Ser Asn Gly Asp Ser Thr Tyr Tyr
2579                      185                 190
2580
2581  CCA GAC ACT GTG AAG GGC CGA TTC ACC ATC 630
2582  Pro Asp Thr Val Lys Gly Arg Phe Thr Ile
2583                      195                 200
2584
2585  TCC AGA GAC AAT GCC AAG AGC ACC CTG GAT 660
2586  Ser Arg Asp Asn Ala Lys Ser Thr Leu Asp
2587                      205                 210
2588
2589  CTG CAA ATG AGC AGT CTG AAG TCT GAG GAC 690
2590  Leu Gln Met Ser Ser Leu Lys Ser Glu Asp
2591                      215                 220
2592
2593  ACA GCC TTG TAT TTC TGT GTA AGA GAG ACT 720
2594  Thr Ala Leu Tyr Phe Cys Val Arg Glu Thr
2595                      225                 230
2596
2597  TAT TAC TAC GGG ATT AGT CCC GTC TTC GAT 750
2598  Tyr Tyr Tyr Gly Ile Ser Pro Val Phe Asp
2599                      235                 240
```

INPUT SET: S8120.raw

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2600
2601   GTC TGG GGC ACA GGG ACC ACG GTC ACC GTC 780
2602   Val Trp Gly Thr Gly Thr Thr Val Thr Val
2603                   245                 250
2604
2605   TCC TCA CTC GAG CAC CAC CAC CAC CAC CAC 810
2606   Ser Ser Leu Glu His His His His His His
2607                   255                 260
2608
2609   TGA                                 813
2610
2611
2612
```

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